NEOsphere
BIOTECHNOLOGIES

neoVERSE
Power TPD drug discovery with proteomic data

neoVERSE. Transform proteomic data into biological knowledge.

Efficient and straightforward analysis of proteomic data is crucial for its immediate application in drug discovery, including target identification and validation, SAR-based compound optimization, compound design, and library expansion.

neoVERSE is a user-friendly, fully automated data analysis suite that provides advanced visualization and analysis tools for the intuitive and interactive exploration of large proteomic datasets. With customizable features and informative dashboards, **neoVERSE** enables comprehensive project evaluation with a single click.

Users can adjust performance parameters to conduct detailed statistical and activity analyses at both the individual compound and project levels. **neoVERSE** also supports extensive meta-analysis and offers tools to assess the biological and clinical relevance of potential degrader target proteins.

Data sharing and export are optimized for seamless integration into drug discovery decision-making. As a web-based application, **neoVERSE** is easily accessible to NEOsphere Biotechnologies' partners for analyzing data from collaborative projects.

The data displayed in **neoVERSE** are generated by integrating advanced data processing software, such as DIA-NN, with NEOsphere Biotechnologies' validated biostatistical pipeline, ensuring the highest standards of data quality and reliability. Our scalable and fully automated DIA-MS data analysis provides exceptional precision, accuracy, completeness, and sensitivity, enabling the swift and simultaneous processing of high-throughput proteomics data with turnaround times tailored to drug discovery needs.

We offer the highest quality statistical analyses, including rigorous quality control for protein identification and quantification, advanced data filtering, proprietary normalization, batch correction, and highly sensitive differential abundance testing using sophisticated linear models.

The data processing and analysis tools developed by NEOsphere Biotechnologies have been extensively tested for consistent reliability and reproducibility across thousands of mass spectrometry runs and samples.

Trained and optimized on > 100,000 samples

> 11,000 proteins per sample

Median CVs of 3-5 %

1% false discovery rate

> 99% data completeness at protein level

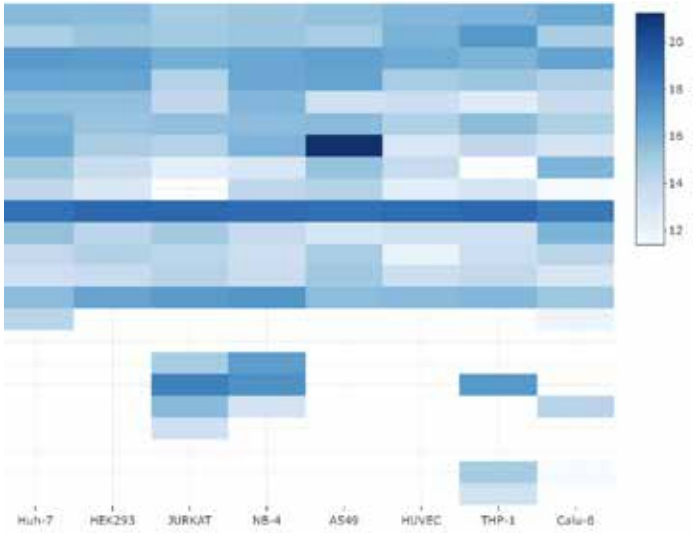

neoVERSE
neoCELL
neoREVIEW
neoCOMPARE
neoID
neoX
neoBIOLOGY
neoSUBSTRATES
neoBASE

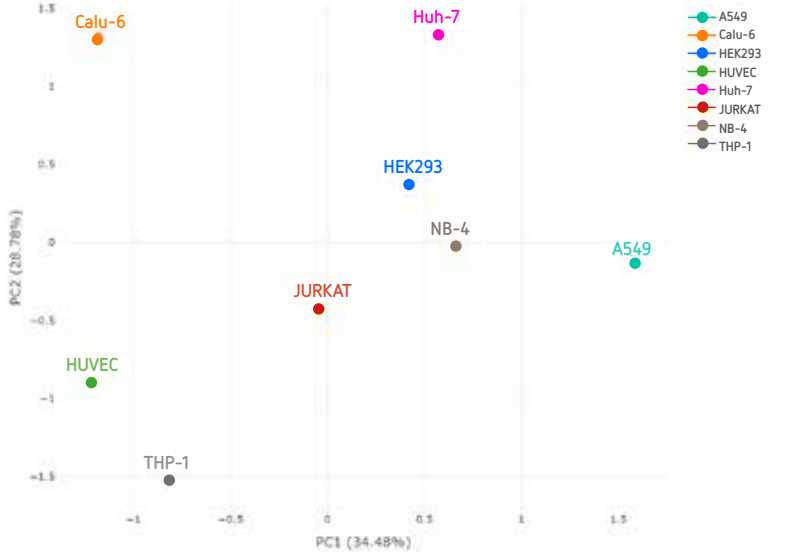
Optimize Your Project Design

neoCELL is a comprehensive database offering unparalleled insights into protein expression across a wide range of cell lines and tissues. It provides detailed information on the abundance, intensity, and half-life of over 15,000 proteins, as well as cellular IMiD responsiveness at the proteome level.

Designed to quickly identify the optimal cell line or tissue for analyzing specific targets or E3 ligases, **neoCELL** also enhances proteome coverage for selectivity or toxicity studies.

neoCELL is fully customizable and can seamlessly integrate additional cell or tissue data upon request to meet our partners' needs.





Search:

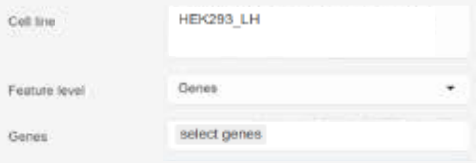
Genes	Huh-7	HEK293	JURKAT	NB-4	A549	HUVEC	THP-1	Calu-6
WIZ	15.79	15.72	14.9	15.21	15.46	15.9	16.06	16.66
ZFP91	14.77	15.37	15.09	15.26	14.9	16.16	17.33	14.85
CSNK1A1	17.21	17.1	16.29	16.65	16.91	16.51	16.04	16.83
PATZ1	16.74	16.75	14.51	16.56	16.8	14.9	15.27	14.57
RAB28	15.57	15.51	14.08	15.94	13.41	13.61	12.57	13.75
ZNF787	16.1	15.35	15.54	15.68	15.72	14.62	15.65	14.6
GZF1	16.48	14.89	14.54	16.03	21.22	12.97	14.03	13.2

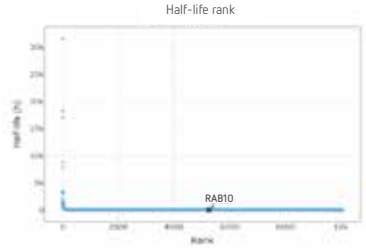
Explore the Impact of Your Drug on Protein Homeostasis

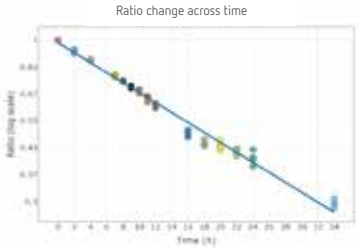
neoCELL also provides quantitative analyses of protein turnover, monitoring proteome-wide protein synthesis and degradation in dynamic systems. This valuable data assists in selecting cell lines for analyzing your target of interest and optimizing drug dosing strategies for proteins with varying synthesis rates.

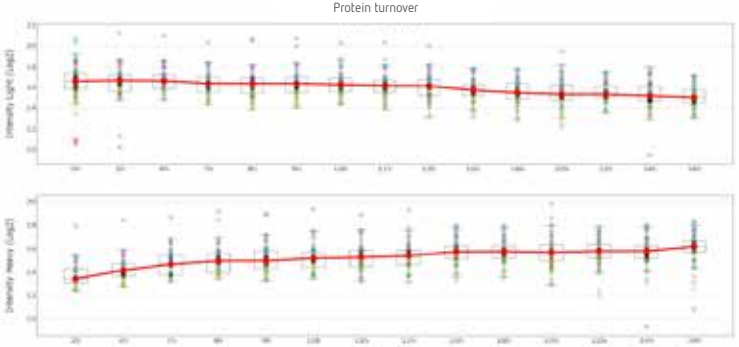
Protein half-lives for over 10,000 proteins are reliably quantified per cell line across multiple timepoints, with accuracy ensured through routine correction for cell doubling time.

neoCELL provides our partners access to extensive protein half-life data across a wide range of cell lines, with analyses of your cell line of interest available anytime.









Protein Turnover in HEK293 cells

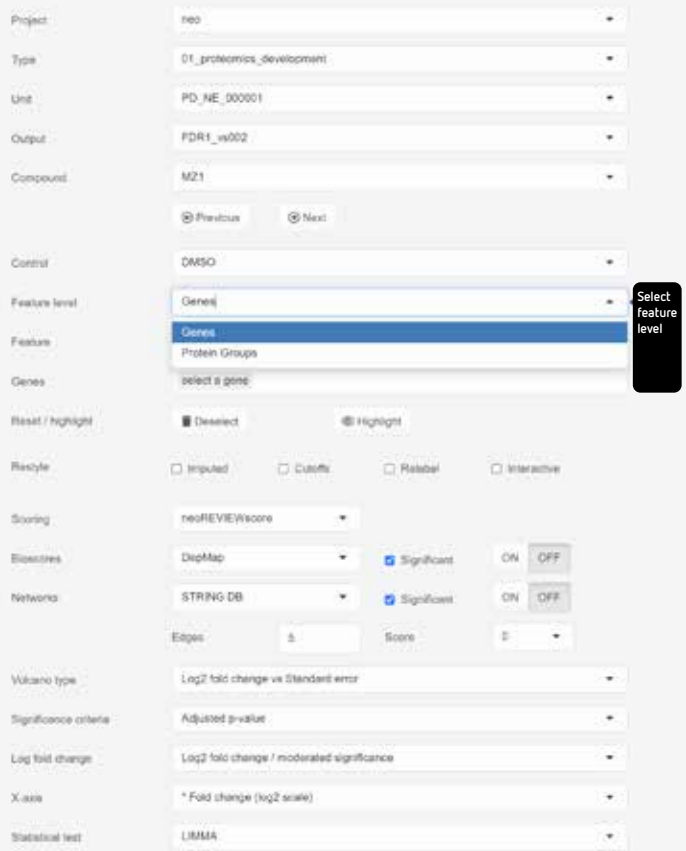
	Genes	Protein groups	Half-life (h)	Half-life (h) adjusted for cell doubling time	R-squared	Degradation constant	Number of time points
1	YTHDF2	Q9Y5A9	12.92	22.17	0.99	-0.05	15/15
2	MARCKSL1	P49006	14.36	26.75	0.99	-0.05	15/15
3	RIF1	Q5UIP0	15	29.08	0.99	-0.04	15/15
4	NUFIP2	Q7Z417&Q7Z417-2	17.24	38.82	0.99	-0.04	15/15
5	GTF21	P78347; P78347-2; P78347-3; P78347-4	17.64	40.94	0.99	-0.04	15/15
6	CEP43	O95684; O95684-2	17.78	41.72	0.99	-0.04	15/15
7	SMC3	Q9UQE7	17.94	42.57	0.99	-0.04	15/15
8	AHSA1	O95433	18.04	43.13	0.99	-0.04	15/15
9	LARP4B	Q92615	18.06	43.24	0.99	-0.04	15/15
10	MARCKS	P29966	18.43	45.45	0.99	-0.04	15/15
11	**RAB10**	**P61026**	**18.7**	**47.16**	**0.99**	**-0.04**	**15/15**
12	UBL4A	P11441	18.73	47.31	0.99	-0.04	15/15

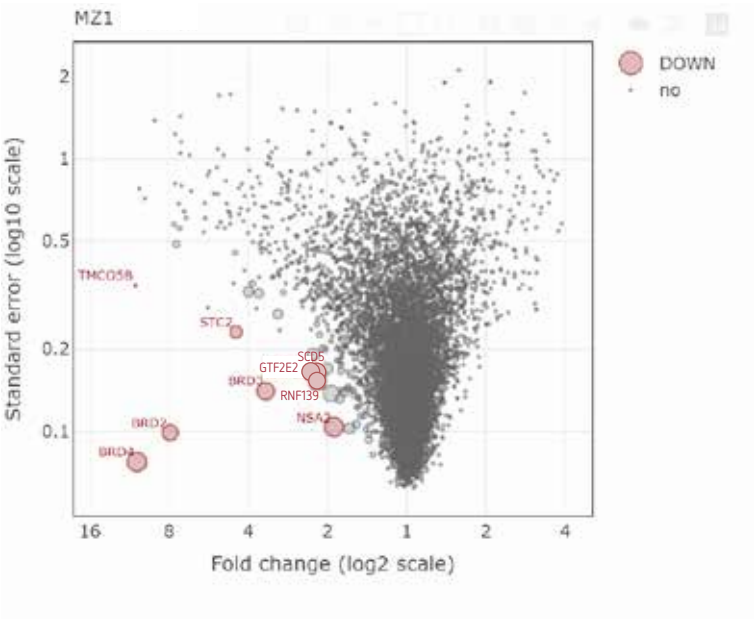
Assess Your Compound Library at a Glance

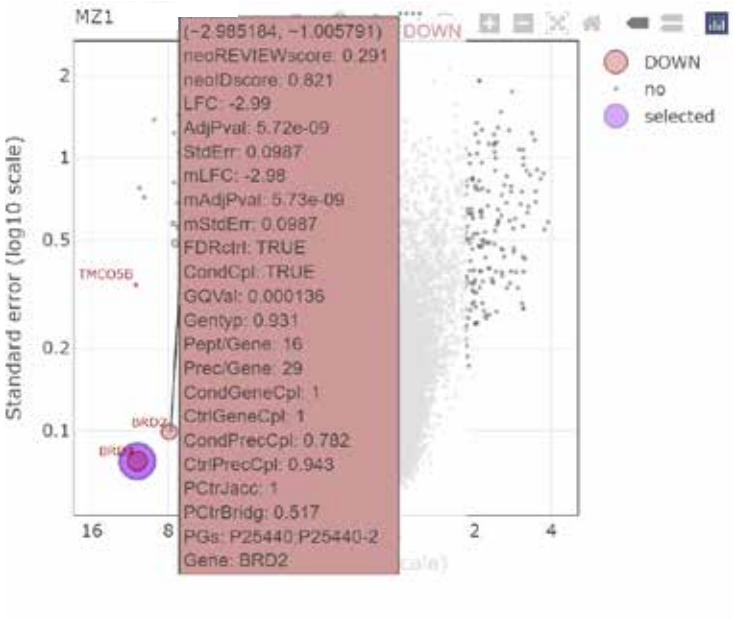
neoREVIEW offers a comprehensive suite of intuitive analysis tools and interactive menus for seamless performance reviews of entire proteomic datasets.

Its detailed statistical evaluations and activity analyses at both the individual compound level and across projects enable effective assessment of efficacy, potency, and specificity for both single compounds and entire compound libraries.

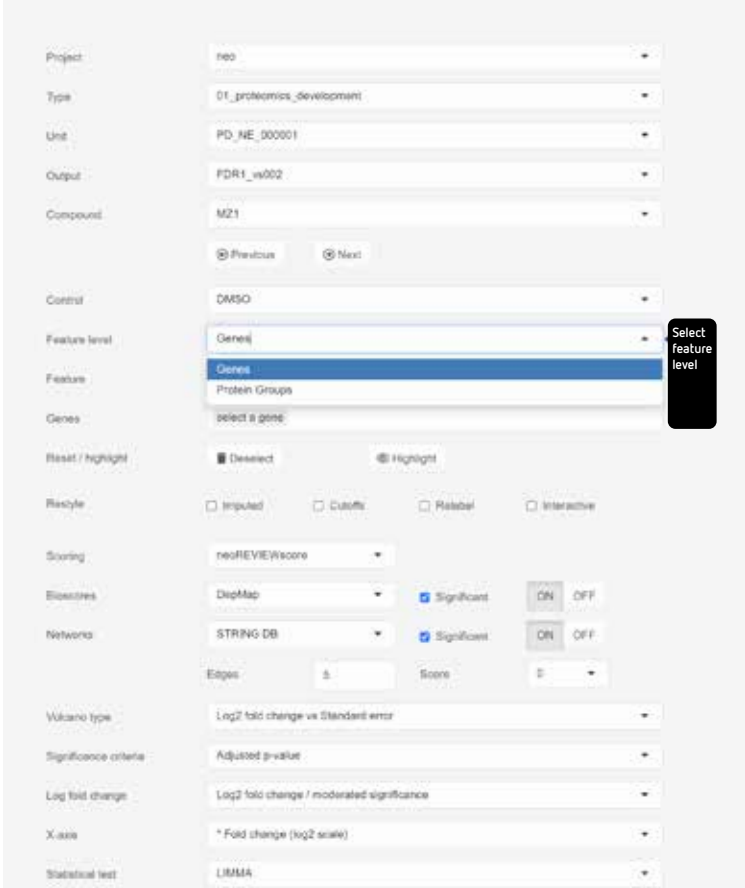
Standard settings facilitate robust analysis, while customizable parameters allow for more in-depth exploration.



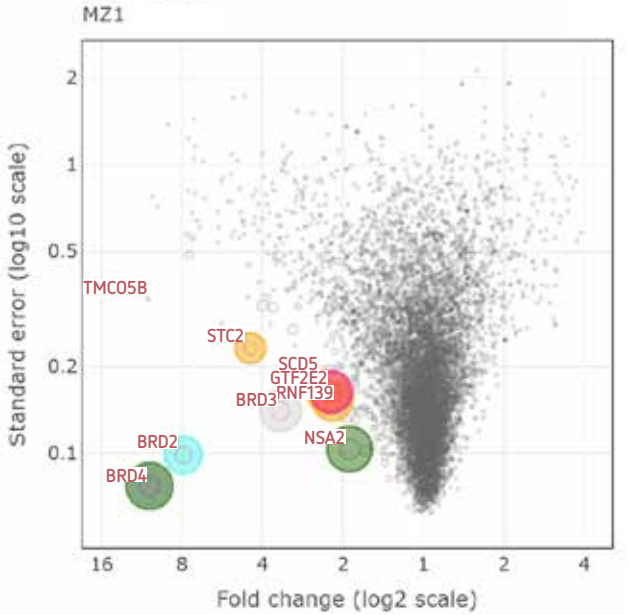


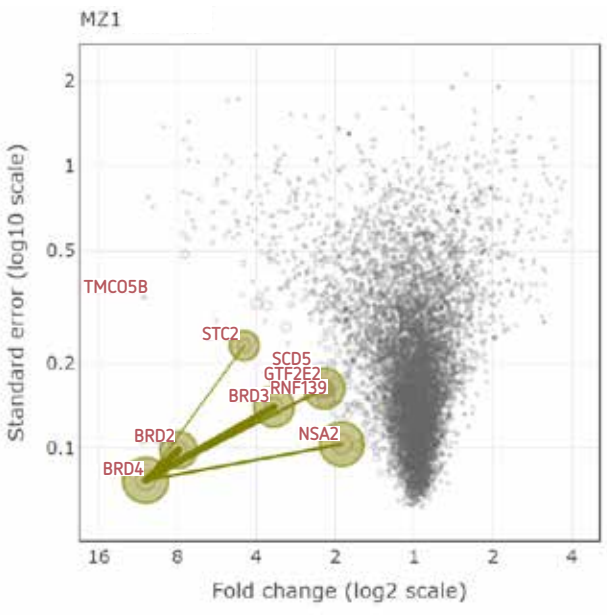


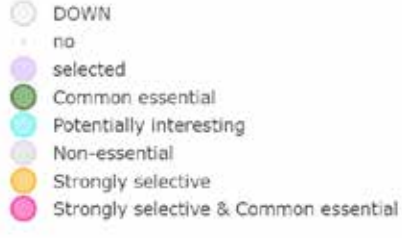
Displayed are volcano plots from a proteomic analysis of HEK293 cells treated with MZ1, a cereblon E3 ligase modulator. The x-axis depicts the fold change (log2) in compound vs. DMSO-treated cells, while the y-axis represents the standard error. Proteins that are significantly down-regulated upon compound treatment are displayed in red. A convenient hover-over functionality allows for the quick evaluation of relevant technical and quality criteria for each detected protein.

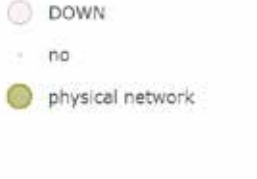

Project
neo
Type
01_proteomics_development
Unit
PD_NE_000001
Output
FDR1_vs002
Compound
M21
Previous
Next
Control
DMSO
Feature level
Genes
Genes
Protein Groups
Select feature level
Feature
Genes
select a gene
Reset / highlight
Deselect
Highlight
Restyle
Imputed
Cutoffs
Relabel
Interactive
Scoring
neoREVIEWscore
Biosetnes
DepMap
Significant
ON
OFF
Networks
STRING DB
Significant
ON
OFF
Edges
5
Score
0
Volcano type
Log2 fold change vs Standard error
Significance criteria
Adjusted p-value
Log fold change
Log2 fold change / moderated significance
X-axis
Fold change (log2 scale)
Statistical test
LIMMA

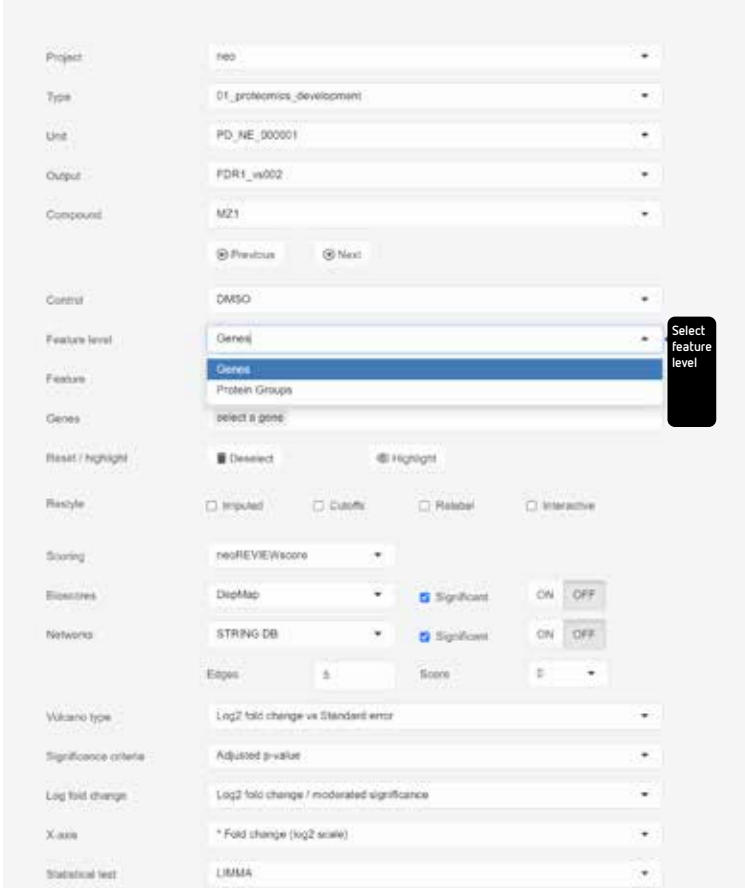
Visualizations include specific annotations, classifications, and protein interactions, along with network information and other relevant details that can be effortlessly integrated into each plot.



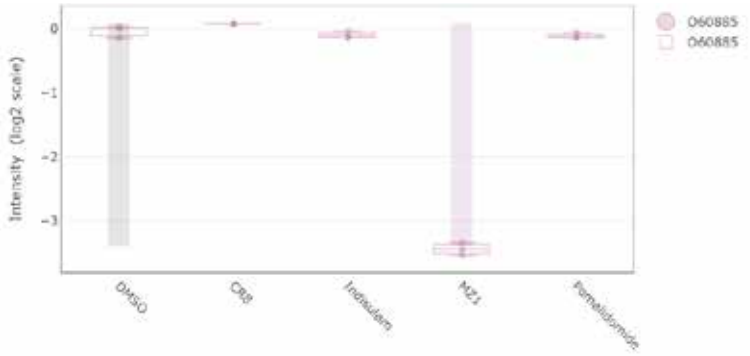




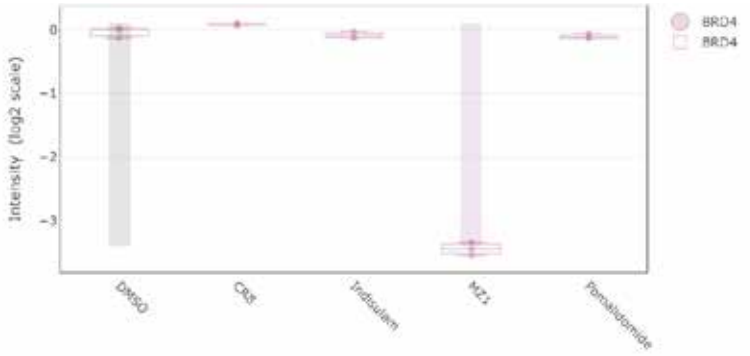



Project
neo
Type
01_proteomics_development
Unit
PD_NE_000001
Output
FDR1_vs002
Compound
M21
Previous
Next
Control
DMSO
Feature level
Genes
Genes
Protein Groups
Select feature level
Feature
Genes
select a gene
Reset / highlight
Deselect
Highlight
Restyle
Imputed
Cutoffs
Relabel
Interactive
Scoring
neoREVIEWscore
Biosetnes
DepMap
Significant
ON
OFF
Networks
STRING DB
Significant
ON
OFF
Edges
5
Score
0
Volcano type
Log2 fold change vs Standard error
Significance criteria
Adjusted p-value
Log fold change
Log2 fold change / moderated significance
X-axis
Fold change (log2 scale)
Statistical test
LIMMA

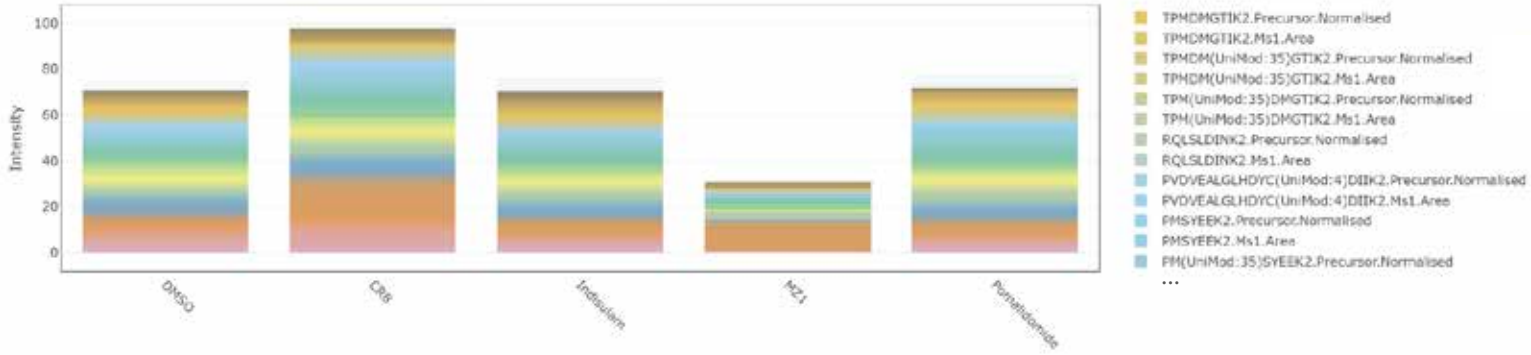
Protein group detail plot (BRD4)



Gene detail plot (BRD4)



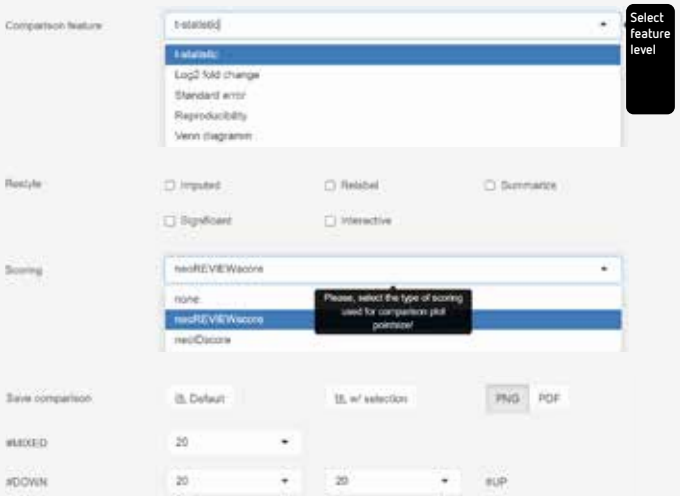
Precursor detail plot (BRD4)



Uncover Key Characteristics of Your Compounds

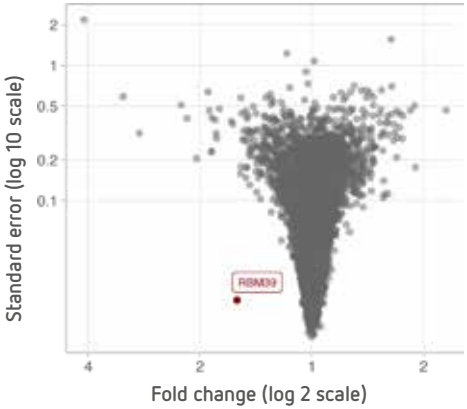
neoCOMPARE provides a structured overview of essential compound characteristics, including proteome-wide target profiles, changes in degradation profiles based on treatment time or concentration, and treatment comparisons between different cells or tissues.

Additionally, it facilitates direct comparisons between diverse experiments, such as global proteomics and ubiquitinomics (as illustrated on the right). This feature allows for the rapid identification of proteins that are simultaneously degraded and ubiquitinated, highlighting potential direct degradation targets.



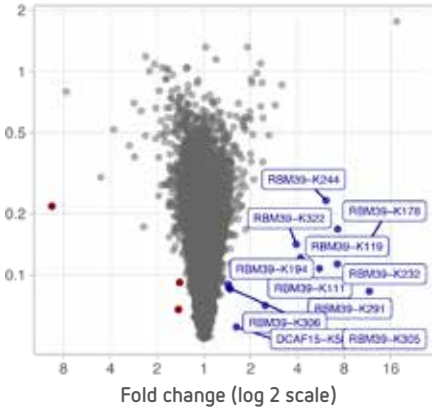
Deep proteomic screening

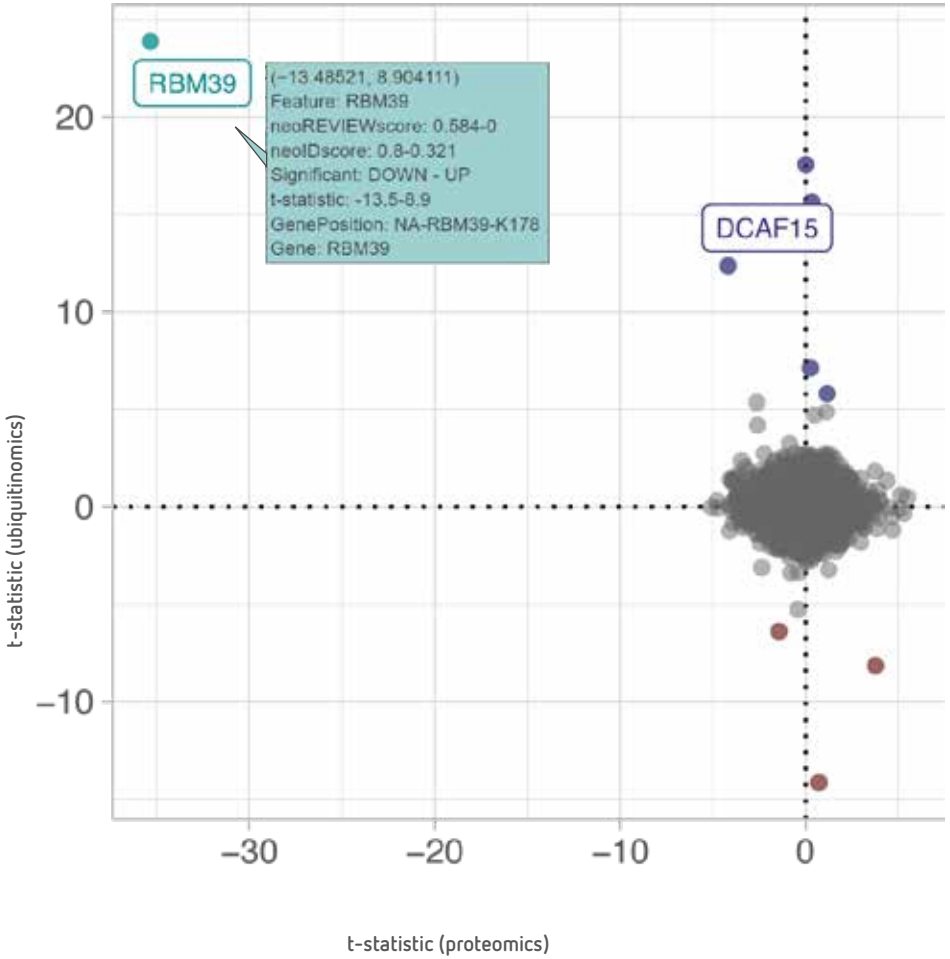
5hrs treatment with Indisulam in HEK293 cells



Global ubiquitinomics

30mins treatment with Indisulam in HEK293 cells





Leverage Proteomic Data for Compound Optimization

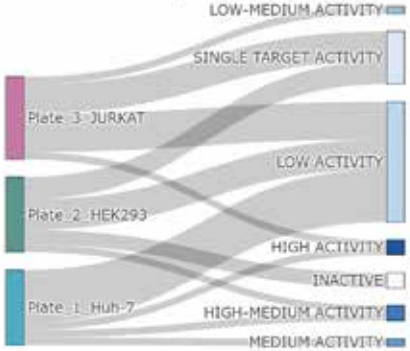
neoID is the fastest and easiest solution for analyzing large proteomics datasets. It enhances drug discovery and SAR-based drug optimization with advanced features and customizable functionalities.

Intuitive dashboards provide a complete project overview or allow users to focus on selected parameters. Interactive visualizations of drug-target interactions generate biological activity maps for entire compound libraries, facilitating the identification of the most active compounds against targets of interest.

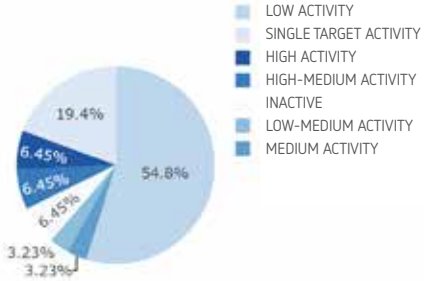
156095 - 200300	10302 - 11126	10130 - 10872	0.995 - 0.996	0.061 - 0.083
PRECURSORS	PROTEIN GROUPS	GENES	COMPLETENESS	COEFFICIENT OF VARIATION

Number of compounds

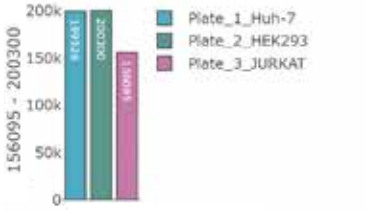
Activity map



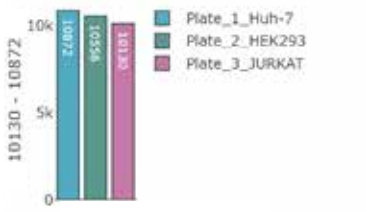
Compound activity



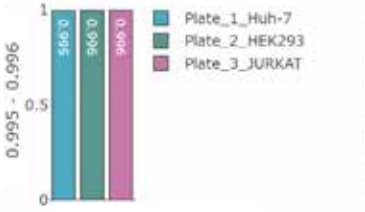
Number of precursors



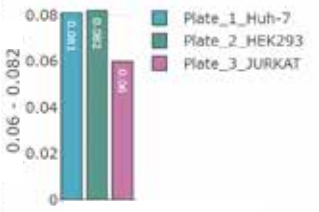
Number of genes



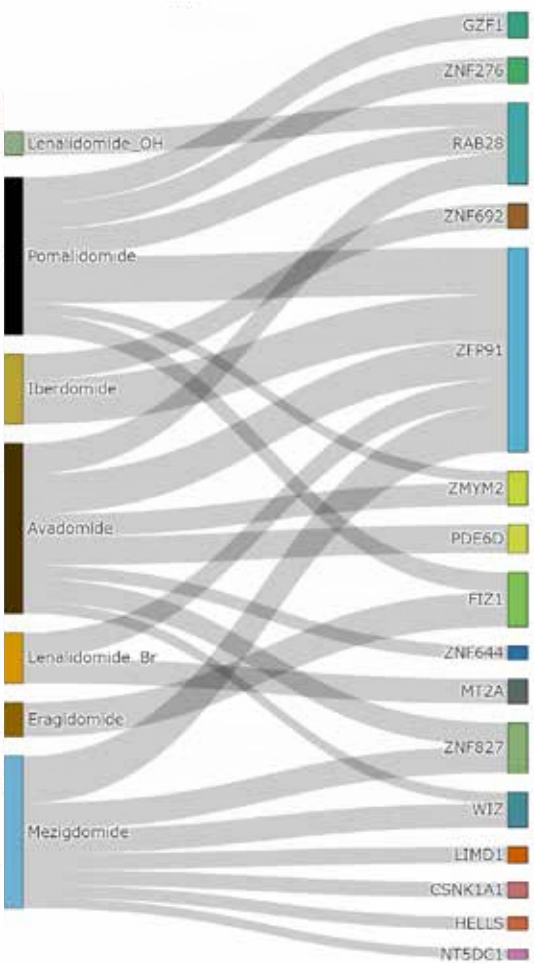
Gene completeness

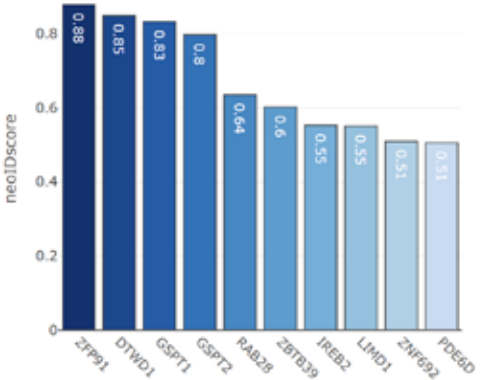


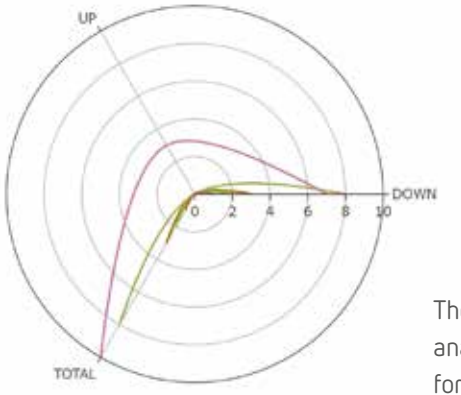
Gene coefficient of variation




Hits
ZFP91 DTWD1 ZBTB39 RAB28
ZNF692 ZNF644 ZMYM2 PDE6D
GSPT1 GSPT2 CSNK1A1 IREB2
WIZ LIMD1 KDM5C
Contrasts
Pomalidomide - DMSO
Avadomide - DMSO
Lenalidomide_5_aminomethyl_HCl - DMSO
CC_885 - DMSO
Scoring
neoIDscore
Scoring level
0.2
Restyle
Imputed
Relabel
Gene-level
Significance criteria
Adjusted p-value
Moderation
yes
P-value
0.01
Fold
1
Focus
select focus
Exclude
select to exclude
Activity classes
SINGLE TARGET ACTIVITY
LOW ACTIVITY





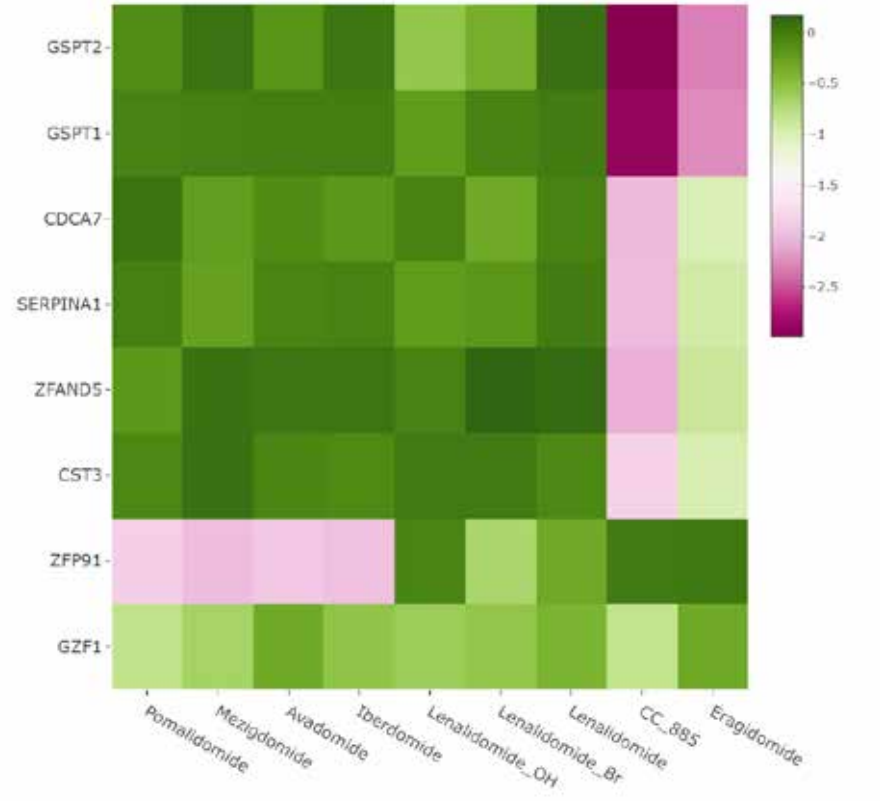


The proteome-wide target scope of the analyzed compounds is displayed, allowing for a quick evaluation of target interactions and statistically significant regulated proteins in a project at a glance.

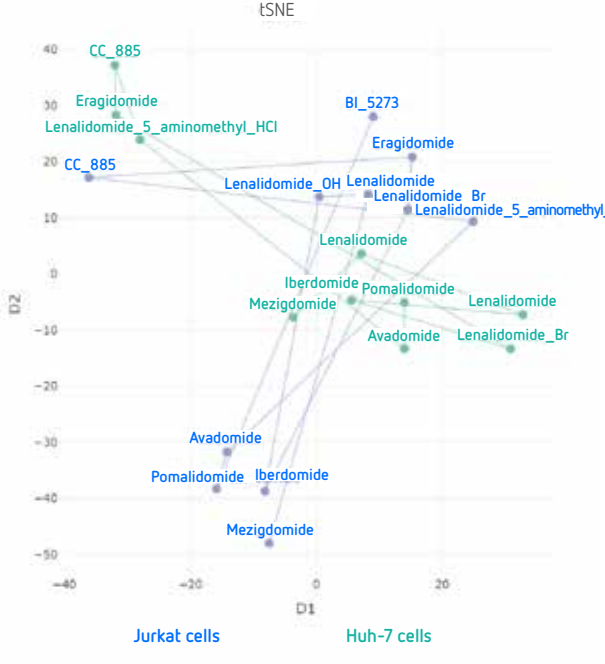
Interpret Complex Data with Ease

neoX simplifies the visualization and meta-analysis of complex, high-dimensional, and large-scale proteomic data, enabling seamless comparison and evaluation across different experiments and projects.

By integrating statistical analysis tools such as PCA (principal component analysis), t-SNE (t-distributed stochastic neighbor embedding), and heat maps, **neoX** identifies patterns, clusters, and specific data points, making them immediately actionable.



Easily visualize how different compounds affect your targets of interest.

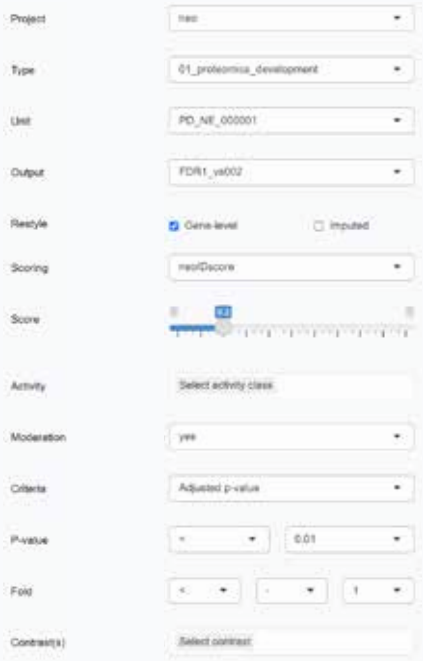


Gain an immediate overview of proteome-wide compound effects across diverse cell lines.

Transform Proteomic Data into Biological Knowledge

neoBIOLOGY swiftly evaluates the biological and clinical significance of proteomically identified target proteins and ubiquitination sites, along with their interactions with tested compounds, thereby unlocking new opportunities for drug discovery.

It leverages a wealth of data sources, including preclinical and clinical data, relevant literature, comprehensive disease and drug databases, and detailed structural information down to the peptide level, for thorough evaluation of potential target proteins.



PROJECT
neo

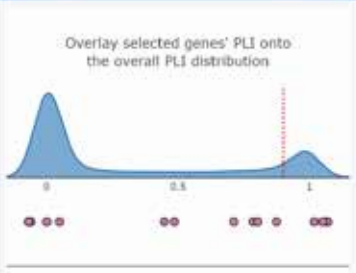
PLATE
PD_NE_000001

NUMBER OF COMPOU...
4

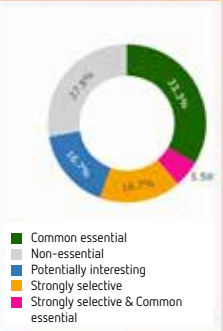
NUMBER OF GENES
19

Select focus
Select gene(s)

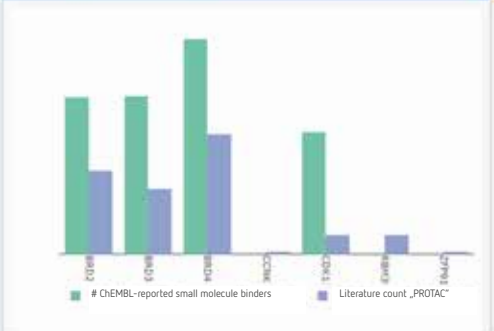
Probability of loss-of-function intolerance (pLI)



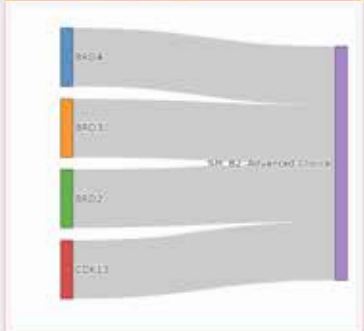
Cancer Dependency Map



PROTAC - literature evidence



Overview of known drugs



Info box

Show 7 entries

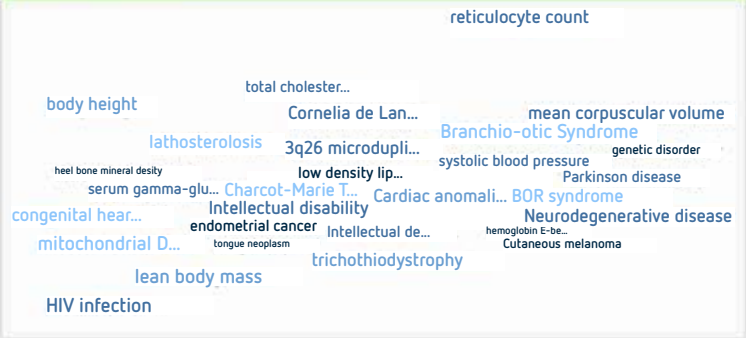
Search:

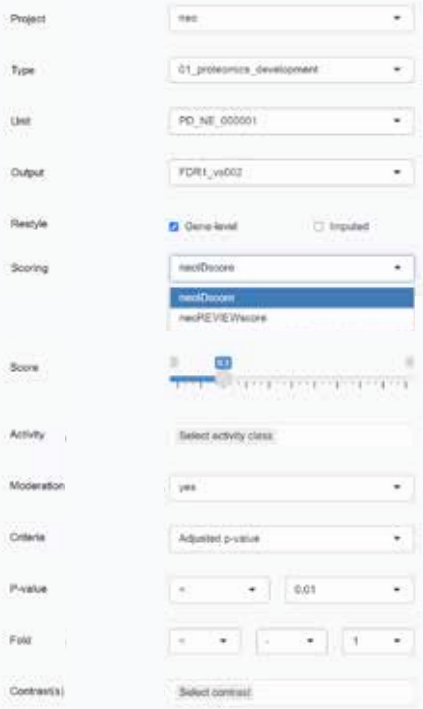
	Gene	Druggable genome member	Ubiquitination [uniprot]	Ubiquitination [database]	Half-life [min-max] h	G-loop
1	NSA2	No	Yes	Yes	13.77-24.19	No
2	CCNK	No	No	Yes	42.16-143.9	No
3	MPV	No	No	Yes	153.3-153.3	No
4	FYTTD1	No	Yes	Yes	11.63-19.69	No

Showing 1 to 7 of 19 entries

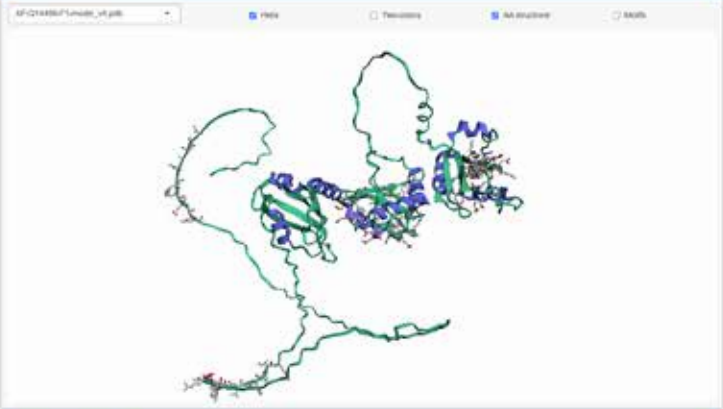
Previous 1 2 3 Next

Target-disease relationship




Project
neo
Type
01_proteomics_development
Unit
PD_NE_000001
Output
FDR1_v0002
Recycle
Gene-level
Imputed
Scoring
neoIDscore
neoIDscore
neoREVIEWscore
Score
0.3
Activity
Select activity class
Moderation
yes
Criteria
Adjusted p-value
P-value
<
0.01
Fold
>
1
Contrast(s)
Select contrast

Alphafold structure



Precursor intensity across samples

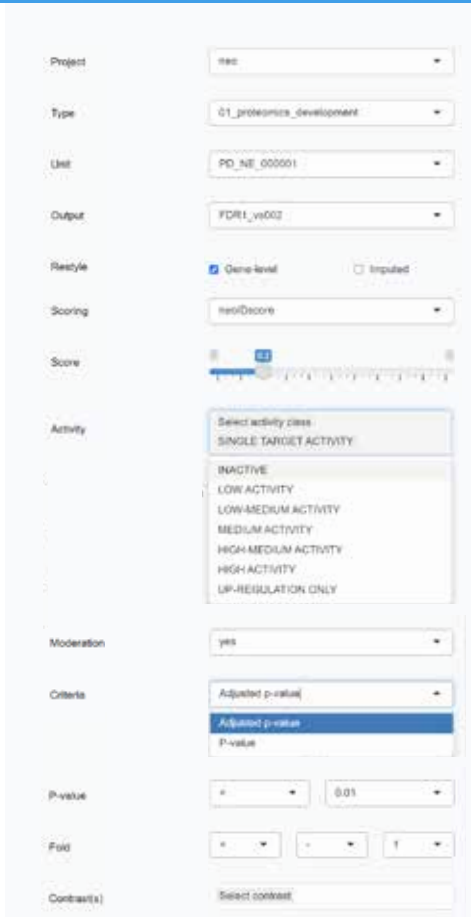
Family & Domains - table

	Start	end	description	type
1	1	1	Removed	Initiator methionine
2	1	146	Disordered	Region
3	2	530	RNA-binding protein 39	Chain
4	2	2	N-acetyalanine	Modified residue
5	2	2	in dbSNP:rs1803701	Natuarl variant
6	9	31	Basic and acidic residues	Compositional bias

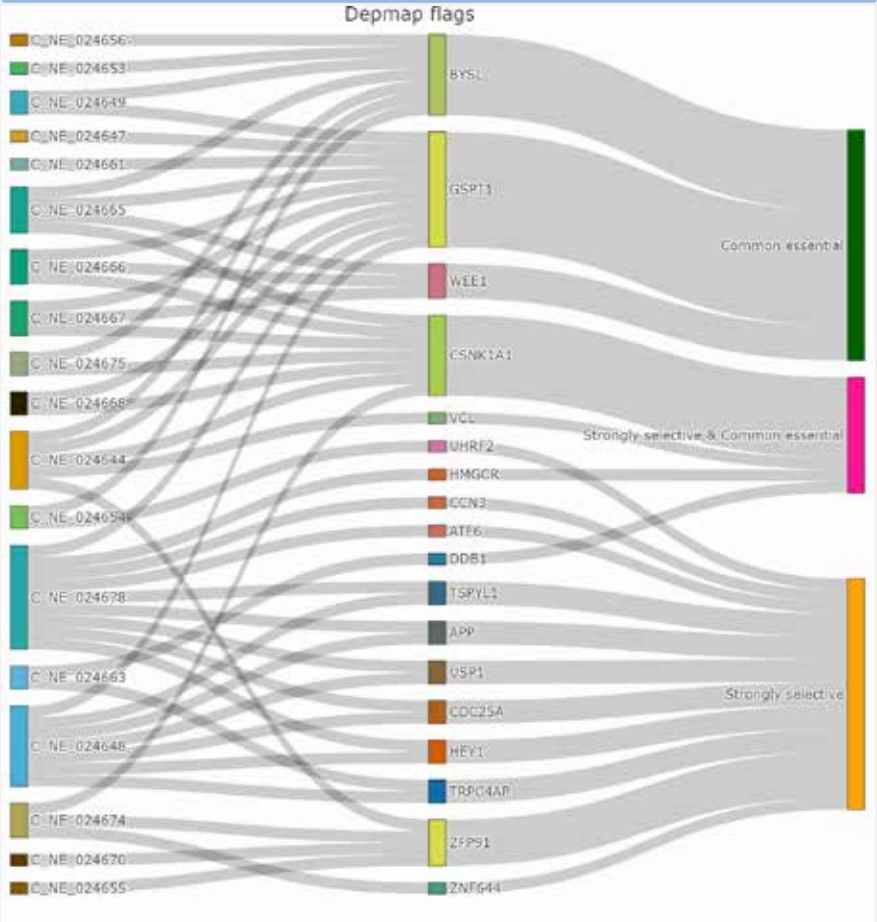
Protein sequence

Degrons

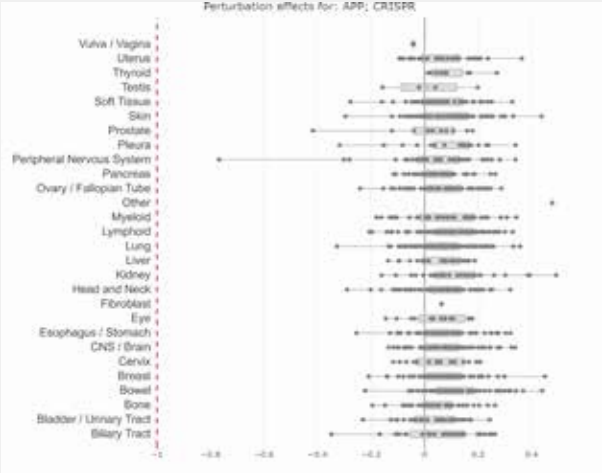
	Degron	Degron loaction	Degron Position	Degron type	Reference [degron]	Known UPS	Refenence [Known UPS]	Licence
1	SFVxxL	Internal	394-400		37738965	MYH11	37738965	CC BY 4.0
2	Wxxxl	Internal	442-447		37738965	LRRC43	37738965	CC BY 4.0
3	Wxxxl	Internal	442-447		37738965	PDZRN3	37738965	CC BY 4.0
4	FVxxL	Internal	395-400	CUL1_FBXO38	37738965	AGRN	37738965	CC BY 4.0


Project
neo
Type
01_proteomics_development
Unit
PD_NE_000001
Output
FDR1_v0002
Recycle
Gene-level
Imputed
Scoring
neoDscore
Score
0.1
Activity
Select activity class
SINGLE TARGET ACTIVITY
INACTIVE
LOW ACTIVITY
LOW-MEDIUM ACTIVITY
MEDIUM ACTIVITY
HIGH-MEDIUM ACTIVITY
HIGH ACTIVITY
UP-REGULATION ONLY
Moderation
yes
Criteria
Adjusted p-value
Adjusted p-value
P-value
P-value
0.01
Fold
Contrast(s)
Select contrast

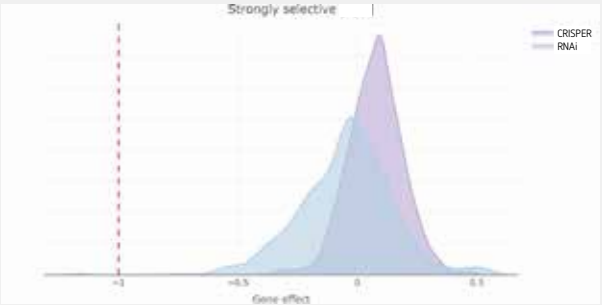
Sankey Plot based on DepMap flags



Perturbation effects across cell-lines



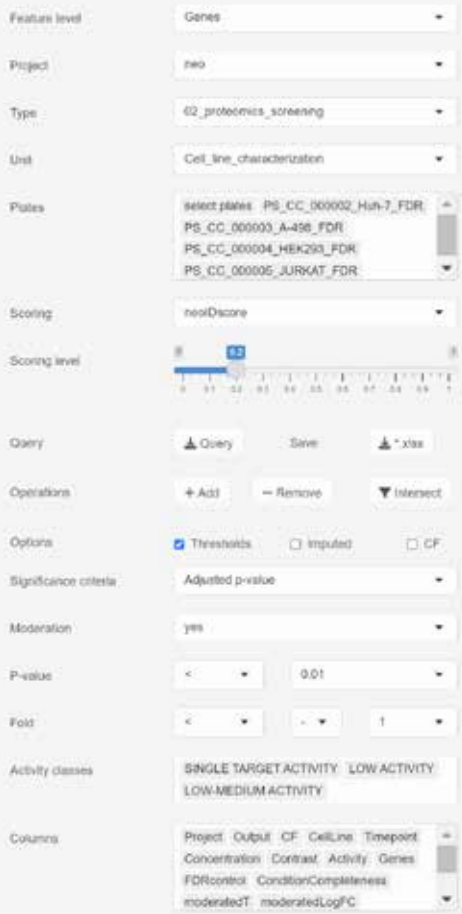
Distribution of scores



All Project Results at a Glance

neoSUBSTRATE is a convenient platform for comparing a wide range of experimental data, enabling the rapid identification of compounds with the highest specificity and sensitivity for target proteins of interest across entire projects.

It facilitates the visualization and comparison of experimental conditions, such as testing compounds in various cells types, at different time points, or across experiments such as proteomics and global ubiquitinomics.



DB query

Show 5 entries Search:

	Project	Output	CF	CellLine	Timepoint	Concentration	Contrast	Activity	Genes	FDRcontrol	ConditionCompleteness	moderatedT	moderatedLogFC	moderat
1	neo	PS_CC_000002_Huh-7_FDR	0	Huh7	2h	10µM	Pomalidomide - DMSO	LOW ACTIVITY	ZFP91	1	1	-17	-1.5	
2	neo	PS_CC_000002_Huh-7_FDR	0	Huh7	2h	10µM	Pomalidomide - DMSO	LOW ACTIVITY	DTWD1	1	1	-6.8	-0.83	
3	neo	PS_CC_000002_Huh-7_FDR	0	Huh7	2h	10µM	Pomalidomide - DMSO	LOW ACTIVITY	RAB28	1	1	-7.5	-0.66	
4	neo	PS_CC_000002_Huh-7_FDR	0	Huh7	2h	10µM	Pomalidomide - DMSO	LOW ACTIVITY	WIZ	1	1	-7.8	-0.26	
5	neo	PS_CC_000002_Huh-7_FDR	0	Huh7	2h	10µM	Pomalidomide - DMSO	LOW ACTIVITY	ZBTB16	1	1	-7.1	-0.79	

Showing 1 to 5 of 104 entries

Previous 1 2 3 4 5 ... 21 Next

CMPD-TARGET scoring

Show 10 entries Search:

	CmpdTargetPair	Genes	CF	neoIDscore	Activity	Nr	Project	Output
29	Mezigdomide - ZFP91	ZFP91	0	1	LOW-MEDIUM ACTIVITY	15	neo	PS_CC
24	Avadomide - RAB28	RAB28	0	0.84	LOW ACTIVITY	9	neo	PS_CC
2	Lenalidomide - CSNK1A1	CSNK1A1	0	0.54	LOW ACTIVITY	8	neo	PS_CC
10	Mezigdomide - IKZF1	IKZF1	0	1	LOW-MEDIUM ACTIVITY	6	neo	PS_CC
26	Mezigdomide - WIZ	WIZ	0	0.84	LOW ACTIVITY	6	neo	PS_CC
3	Avadomide - DTWD1	DTWD1	0	0.76	LOW ACTIVITY	5	neo	PS_CC
6	CC_885 - GSPT1	GSPT1	0	0.66	LOW ACTIVITY	5	neo	PS_CC
12	Mezigdomide - IKZF3	IKZF3	0	1	LOW-MEDIUM ACTIVITY	4	neo	PS_CC
28	Avadomide - ZBTB39	ZBTB39	0	0.59	LOW ACTIVITY	4	neo	PS_CC
30	Avadomide - ZMYM2	ZMYM2	0	0.53	LOW ACTIVITY	4	neo	PS_CC

Showing 1 to 10 of 36 entries

Previous 1 2 3 4 Next

Show 10 entries Search:

	CmpdTargetPair	Genes	CF	neoIDscore	Activity	CellLine	Timepo
1	Lenalidomide_OH - CSNK1A1	CSNK1A1	0	0.5	LOW ACTIVITY	Huh7	2h
2	Lenalidomide - CSNK1A1	CSNK1A1	0	0.54	LOW ACTIVITY	Huh7	2h
3	Mezigdomide - CSNK1A1	CSNK1A1	0	0.54	LOW ACTIVITY	Huh7	2h
4	Mezigdomide - CSNK1A1	CSNK1A1	0	0.24	LOW-MEDIUM ACTIVITY	JURKAT	5h
5	Lenalidomide_OH - CSNK1A1	CSNK1A1	0	0.31	LOW ACTIVITY	JURKAT	5h
6	Lenalidomide_OH - CSNK1A1	CSNK1A1	0	0.42	SINGLE TARGET ACTIVITY	HEK293	5h
7	Lenalidomide - CSNK1A1	CSNK1A1	0	0.35	SINGLE TARGET ACTIVITY	HEK293	5h
8	Mezigdomide - CSNK1A1	CSNK1A1	0	0.49	LOW ACTIVITY	HEK293	5h

Showing 1 to 8 of 8 entries

Previous 1 Next

Tailored Statistical Analysis for Your Needs

neoBASE is a sophisticated database that facilitates interactive querying of all statistical metrics relevant to large-scale proteomic data analysis.

Key statistical parameters - such as p-value, fold change, FDR control, and t-statistical evaluations - can be displayed across projects and at various levels including genes, proteins, or peptides. Threshold values and default settings are easily adjustable, allowing for thorough data evaluation tailored to your specific needs.

Show 20 entries

Search: CC_00000

	Project	Output	CF	CellLine	Timepoint	Concentration	Contrast	Genes	FDRcontrol	ConditionCompleteness	moderatedT	moderatedL
138	neo	PS_CC_000006_SK-MEL-30_FDR	0	SK-MEL-30	5h	10µm	Mezigdomide - DMSO	ZFP91	true	true	-22	
139	neo	PS_CC_000005_JURKAT_FDR	0	Jurkat	5h	10µm	Mezigdomide - DMSO	ZFP91	true	true	-44	
140	neo	PS_CC_000005_JURKAT_FDR	0	Jurkat	5h	10µm	Iberdomide - DMSO	ZFP91	true	true	-31	
141	neo	PS_CC_000004_HEK293_FDR	0	HEK293	5h	10µm	Pomalidomide - DMSO	ZFP91	true	true	-16	
142	neo	PS_CC_000004_HEK293_FDR	0	HEK293	5h	10µm	Iberdomide - DMSO	ZFP91	true	true	-20	
143	neo	PS_CC_000004_HEK293_FDR	0	HEK293	5h	10µm	Mezigdomide - DMSO	ZFP91	true	true	-14	
144	neo	PS_CC_000002_Huh-7_FDR	0	Huh-7	2h	10µm	Pomalidomide - DMSO	ZFP91	true	true	-17	
145	neo	PS_CC_000002_Huh-7_FDR	0	Huh-7	2h	10µm	Avadomide - DMSO	ZFP91	true	true	-19	
146	neo	PS_CC_000002_Huh-7_FDR	0	Huh-7	2h	10µm	Iberdomide - DMSO	ZFP91	true	true	-18	
147	neo	PS_CC_000001_PC-3_FDR	0	PC-3	5h	10µm	Pomalidomide - DMSO	ZFP91	true	true	-24	
148	neo	PS_CC_000001_PC-3_FDR	0	PC-3	5h	10µm	Avadomide - DMSO	ZFP91	true	true	-18	
149	neo	PS_CC_000001_PC-3_FDR	0	PC-3	5h	10µm	Iberdomide - DMSO	ZFP91	true	true	-25	
150	neo	PS_CC_000001_PC-3_FDR	0	PC-3	5h	10µm	Mezigdomide - DMSO	ZFP91	true	true	-26	
151	neo	PS_CC_000003_A-498_FDR	0	A498	5h	10µm	Mezigdomide - DMSO	ZFP91	true	true	-15	

Showing 1 to 14 of 14 entries (filtered from 151 total entries)

Previous 1 Next

About NEOsphere Biotechnologies

We are the leading partner in TPD proteomics for pharmaceutical and biotechnology companies, dedicated to support drug discovery and development of comprehensive, innovative degrader pipelines. Our platform integrates advanced mass spectrometry technologies with cutting-edge biostatistical data analysis, enabling high-throughput proteomic screening of entire degrader libraries and robust mechanistic target validation. We offer unmatched sensitivity, precision, and turnaround times, empowering the identification of novel degrader targets and systematically exploring previously undruggable therapeutic spaces.

NEOsphere Biotechnologies GmbH
Fraunhoferstrasse 1
82152 Planegg, Germany
www. neospherebiotechnologies.com
info@neospherebiotech.com